EXTRACELLULAR SERINE PROTEASE

Cross-reference to Related Applications

This patent application is a continuation-in-part of U.S. application 09/796,294 filed February 28, 2001, which is a continuation-in-part of U.S. application 09/618,259 filed July 18, 2000, which is a continuation-in-part of U.S. application 09/137,944 filed August 21, 1998, which is a continuation-in-part of U.S. application 08/915,659 filed August 21, 1997.

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates generally to the fields of cellular biology and the diagnosis of neoplastic disease. More specifically, the present invention relates to a novel extracellular serine protease termed Tumor Antigen Derived Gene-14 (TADG-14).

Description of the Related Art

Serine proteases comprise a family of protein degrading enzymes that serve a host of biological functions including activation of blood coagulation cascades, activation of growth and angiogenic factors and degradation of extracellular matrix components (1-4). In recent years, aberrant expression of serine proteases, such as plasminogen activator have been shown to correlate positively with the invasiveness and metastatic potential of tumor cells (3, 5-6). Presumably, this occurs by increasing the ability of the tumors to degrade extracellular matrix components either directly or indirectly through the proteolytic activation of other zymogenic proteases. More significantly, the serine protease

known as the prostate specific antigen (PSA) has been used successfully as a tumor marker for the early diagnosis of prostate cancer due to its abnormal prevalence in the peripheral blood of these patients (7). Serine proteases play important roles in the cascade of events involved in the malignant process, and at least for prostate cancer, they provide sufficient signal to allow detection of early disease.

The prior art is deficient in the lack of effective means of screening to identify proteases overexpressed in carcinoma. The present invention fulfills this longstanding need and desire in the art.

SUMMARY OF THE INVENTION

The present invention discloses a 1343 base pairs long TADG-14 cDNA (SEQ ID No: 6) which encodes a 260 amino acid protein (SEQ ID No: 7) overexpressed in carcinoma. The availability of the TADG-14 gene opens the way for a number of studies that can lead to various applications.

In one embodiment of the present invention, there is provided a DNA encoding a TADG-14 protein having the amino acid sequence of SEQ ID NO. 7, a vector capable of expressing the DNA of the present invention, as well as host cell transfected with the vector that express the TADG-14 protein. Additionally embodied is a vector in which the TADG-14 DNA is positioned in reverse orientation relative to the regulatory elements such that a TADG-14 antisense DNA is produced.

In another embodiment of the present invention, there is provided a DNA encoding a TADG-14 variant protein having the amino acid sequence of SEQ ID NO. 75 or fragments thereof, a vector capable of expressing said DNA, as well as host cell transfected with the vector that express the TADG-14 variant protein. The TADG-14 protein variant has a potential role for detecting and targeting of ovarian carcinomas.

The present invention also provides an isolated and purified TADG-14 protein (SEQ ID No: 7) and an isolated and purified TADG-14 variant protein (SEQ ID No: 75) or fragments of either protein. The present invention also provides antibodies or antibody fragments specific for the TADG-14 protein or the TADG-14 variant protein.

In another embodiment of the present invention, there are provided methods of using oligonucleotide probe, antibody or antibody fragments to detect TADG-14 mRNA, TADG-14 variant mRNA, TADG-14 protein, or TADG-14 variant protein in a biological sample. Generally, the sample is a biological sample from blood, interstitial fluid, ascites fluid, tumor tissue biopsy or circulating tumor cells. Preferably, the biological sample is from an individual; and typically, the individual is suspected of having cancer.

The present invention also provides kits for detecting TADG-14 mRNA, TADG-14 variant mRNA, TADG-14 protein, or TADG-14 variant protein. The kits comprises oligonucleotide probe, antibody or antibody fragments specific for TADG-14 or TADG-14 variant. The kits can further comprise a label for detecting the probe or antibody.

In yet another embodiment of the present invention, there is provided methods of inhibiting expression of TADG-14 in a cell with TADG-14 antisense DNA or TADG-14-specific antibody. Generally, the inhibition of TADG-14 expression is for treating cancer.

In another embodiment of the present invention, there is provided a method of targeted therapy to an individual, comprising

the step of: (a) administering a compound containing a targeting moiety and a therapeutic moiety to an individual, wherein the targeting moiety is specific for TADG-14.

In another embodiment of the present invention, there are provided methods of diagnosing cancer in an individual through the detection of TADG-14 or TADG-14 variant at the protein or DNA level.

In yet another embodiment of the present invention, there is provided a method of vaccinating an individual against TADG-14 protein, comprising the step of (a) inoculating an individual with a TADG-14 protein or fragment thereof which lacks TADG-14 protease activity. Typically, inoculation with the TADG-14 protein or fragment thereof elicits an immune response in the individual, thereby vaccinating the individual against TADG-14. Generally, the individual has cancer, is suspected of having cancer or is at risk of getting cancer. Preferably, the TADG-14 fragment is a 9-residue fragment up to a 20-residue fragment, and more preferably, the 9-residue fragment is SEQ ID Nos. 17, 18, 41, 42, 47, 48, 53, 56, or 64.

In another embodiment of the present invention, there is provided a method of producing activated immune cells directed

toward TADG-14, comprising the steps of exposing immune cells to a TADG-14 protein or fragment thereof which lacks TADG-14 protease activity. Usually, exposure to the TADG-14 protein or fragment thereof activates the immune cells, thereby producing activated immune cells directed toward TADG-14. Generally, the immune cells are B cells, T cells or dendritic cells. Preferably, the dendritic cells are isolated from an individual prior to exposure to a TADG-14 protein or fragment thereof, and then reintroduced into the individual subsequent to the exposure. Typically, the individual has cancer, is suspected of having cancer or is at risk of getting cancer. Preferably, the TADG-14 fragment is a 9-residue fragment up to a 20-residue fragment, and more preferably, the 9-residue fragment is SEQ ID Nos. 17, 18, 41, 42, 47, 48, 53, 56, or 64.

In another embodiment of the present invention, there is provided an immunogenic composition, comprising an immunogenic fragment of a TADG-14 protein and an appropriate adjuvant. Preferably, the TADG-14 fragment is a 9-residue fragment up to a 20-residue fragment, and more preferably, the 9-residue fragment is SEQ ID Nos. 17, 18, 41, 42, 47, 48, 53, 56, or 64.

In another embodiment of the present invention, there is provided an oligonucleotide having a sequence complementary to

SEQ ID No. 6, as well as a composition comprising the oligonucleotide and a physiologically acceptable carrier. Additionally, there is provided a method of treating a neoplastic state in an individual in need of such treatment, comprising the step of (a) administering to the individual an effective dose of the above-described oligonucleotide.

Other and further aspects, features, and advantages of the present invention will be apparent from the following description of the presently preferred embodiments of the invention given for the purpose of disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a comparison of PCR products derived from normal and carcinoma cDNA as shown by staining in an agarose gel. Two distinct bands (lane 2) were present in the primer pair sense-His-antisense Asp (AS1) and multiple bands of about 500 base pairs are noted in the carcinoma lane for the sense-His antisense-Ser (AS2) primer pairs (lane 4).

Figure 2 shows the Northern blot analysis of TADG-14. **Figure 2A** shows messenger RNA isolated from the tissues of interest was subjected to Northern hybridization using a random labeled 230 bp TADG-14 specific RT-PCR product. The blot was stripped and probed for β-tubulin. **Figure 2B, 2C, and 2D** show multiple tissue Northern blots (Clontech) probed with the same TADG-14 and β-tubulin specific RT-PCR products. TADG-14 mRNA was detected as a 1.4-kb transcript in tumors but not in any normal tissue studied.

Figure 3 shows the cDNA and deduced amino acid sequences of TADG-14 and comparison of predicted TADG-14 sequence with known proteases. **Figure 3A** shows the cDNA sequence of TADG-14 with its deduced 260 amino acid sequence represented by the one-letter code for each residue. Within the cDNA, the underlined portions represent the Kozak's consensus sequence for initiation of translation and the polyadenylation signal, respectively. The TADG-14 protein sequence contains a secretion signal sequence near its amino terminus. The stop codon is represented by the (*) symbol.

Figure 3B shows the amino acid sequence of TADG-14 compared to human glandular kallikrein (hHk2, accession #

P06870), human PSA (hPSA, accession # P07288), mouse neuropsin (mNeur, accession # D30785) and human Protease M (hProM, accession # U62801) using the GCG PILEUP program (REF). The positions of the residues of the catalytic triad are marked Y.

Figure 4 shows a comparison of the amino acid sequence of TADG-14's catalytic domains.

Figure 5 shows the TADG-14 quantitative PCR. **Figure 5A** shows the typical results of a TADG-14 quantitative PCR experiment. The reaction products were electrophoresed through a 2% agarose TAE gel and stained with ethidium bromide. In this figure, the 454-bp band represents the β-tubulin product and the 230-bp band represents the TADG-14 product. The radiolabeled PCR products were quantitated.

Figure 5B shows the overexpression of TADG-14. As determined by the student's t test, TADG-14 mRNA expression levels were significantly elevated in LMP tumors (*, $P=0.05$) and carcinomas ($P<0.0001$) compared to levels found in normal ovary. Individual cases are represented in a scatter plot. This is indicative of heterogeneity of TADG-14 expression among these tumor samples.

Figure 6 shows the TADG-14 expression in tumors and cell lines.

Figure 7 shows Western blot analysis of TADG-14. Polyclonal antibodies were generated by immunization of rabbits with one of three poly-lysine linked multiple antigen peptides derived from the deduced amino acid sequence of TADG-14. For Western blot analysis, approximately 20ug of MDA-MB-435S and HeLa cell lysates were separated on a 15% SDS-PAGE gel and electroblotted to PVDF at 100V for 40 minutes at 4 C. The blot was blocked overnight in Tris-buffered saline (TBS), pH 7.8 containing 0.2% non-fat milk. Primary antibody was added to the membrane at a dilution of 1:100 in 0.2% milk/TBS and incubated for 2 hours at room temperature. The blot was washed and incubated with 1:3000 dilution of alkaline-phosphatase conjugated goat and anti-rabbit IgG antibody (Bio-Rad) for one hour at room temperature. The blot was washed and incubated with a chemiluminescent substrate (Bio-Rad) before a 10-second exposure to X-ray film for visualization.

Figure 8 shows immunohistochemistry of TADG-14. Staining was with the TADG-14-1 antibody for normal ovary, two serous carcinomas, mucinous carcinoma, endometrioid carcinoma and clear cell carcinoma of the ovary (**Figure 8A, Figure 8B,**

Figure 8C, **Figure 8D**, **Figure 8E** and **Figure 8F**, respectively). No staining was observed in normal ovary. The serous carcinoma shown in **Figure 8B** has TADG-14 most strongly associated with the surface of the tumor, while in the serous tumor in **Figure 8C**, TADG-14 was found in a granular form in an apparent secretion pathway. In mucinous carcinoma TADG-14 appears to be most highly expressed along the invasive front of the tumor. TADG-14 was secreted into the lumen of the glandular structure formed by the endometrioid carcinoma in **Figure 8E**. The clear cell carcinoma stained in **Figure 8F** shows diffuse staining throughout all tumor cells.

Figure 9 shows the expression of TADG-14 and T-14 variant in normal ovary and ovarian carcinoma.

Figure 10 presents a diagram of transcript and open reading frame of TADG-14 and TADG-14 variant including intron 2.

Figure 11 shows amino acid sequence comparison of TADG-14 and TADG-14 variant.

DETAILED DESCRIPTION OF THE INVENTION

All serine proteases contain conserved histidine, aspartate and serine residues that are necessary for enzymatic activity. To identify the expressed serine proteases in carcinoma, degenerate oligodeoxynucleotide primers designed to the conserved amino acid sequences surrounding the invariant His and Ser residues of the catalytic triad (8) were used in PCR reactions with cDNA from either normal ovarian tissue or ovarian carcinoma as the template. PCR products of the appropriate size were subcloned into T-vector and sequenced. Previously, this strategy has proved successful in identifying the serine proteases hepsin and stratum corneum chymotryptic enzyme (SCCE) which have been shown to be expressed at abnormally high levels in ovarian carcinoma (9, 10).

Homology searches revealed that one of the subclones obtained from ovarian carcinoma represented a novel 406 base pair (bp) sequence that has significant sequence similarity to other known proteases including mouse neuropsin, human glandular kallikrein and human PSA. The complete cDNA for this novel

sequence was cloned and found to encode a trypsin like serine protease, named TADG-14. The TADG-14 cDNA is 1343 base pairs long (SEQ ID No: 6) and encoding for a 260 amino acid protein (SEQ ID No: 7).

The availability of the TADG-14 gene opens the way for a number of studies that can lead to various applications. More importantly, the TADG-14 transcript was found to be highly expressed in a majority of ovarian tumors but not expressed by normal ovarian tissue. High level expression of TADG-14 appears to be restricted to tumors, and this protease appears to be secreted in a manner that would suggest a possible role in invasion and metastasis. Moreover, due to the extracellular nature of this enzyme, it may be possible to exploit its expression as a diagnostic tool for ovarian cancer.

The present invention also discloses a TADG-14 variant that includes intron sequence between exon 2 and exon 3. This TADG-14 variant could be translated into an extended amino acid sequence which presumably would still have protease activity (Figures 10-11). The addition of the intron sequence and the subsequent translation into additional amino acid sequence provides an opportunity to add unique specificity for diagnostic detection

and/or targeting of tumor therapy. This variant was expressed in 5 out of 6 ovarian carcinomas examined. Normal ovary cells did not express this TADG-14 variant.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D.N. Glover ed. 1985); "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription and Translation" [B.D. Hames & S.J. Higgins eds. (1984)]; "Animal Cell Culture" [R.I. Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press, (1986)]; B. Perbal, "A Practical Guide To Molecular Cloning" (1984).

The amino acids described herein are preferred to be in the "L" isomeric form. However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional property is retained by the polypeptide. It should be noted that all amino-acid residue sequences are represented

herein by formulae whose left and right orientation is in the conventional direction of amino-terminus to carboxy-terminus.

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

The term "oligonucleotide", as used herein in referring to the probe of the present invention, is defined as a molecule comprised of two or more ribonucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

A cell has been "transformed" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. The transforming DNA may or may not be integrated

(covalently linked) into the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transforming DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in which the transforming DNA has become integrated into a chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transforming DNA. A "clone" is a population of cells derived from a single cell or ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

As used herein, the term "host" is meant to include not only prokaryotes but also eukaryotes such as yeast, plant and animal cells. A recombinant DNA molecule or gene which encodes a human TADG-14 protein of the present invention can be used to transform a host using any of the techniques commonly known to those of ordinary skill in the art. Especially preferred is the use of a vector containing coding sequences for the gene which encodes a human TADG-14 protein of the present invention for purposes of prokaryote transformation.

Prokaryotic hosts may include *E. coli*, *S. tymphimurium*, *Serratia marcescens* and *Bacillus subtilis*. Eukaryotic hosts include yeasts such as *Pichia pastoris*, mammalian cells and insect cells.

The invention includes a substantially pure DNA encoding a TADG-14 protein, containing a sequence of at least 15 consecutive nucleotides (preferably 20, more preferably 30, even more preferably 50, and most preferably all) of the region from nucleotides 1 to 1343 of the nucleotides listed in SEQ ID NO: 6. The protein encoded by the DNA of this invention may share at least 80% sequence identity (preferably 85%, more preferably 90%, and most preferably 95%) with the amino acids listed in SEQ ID NO: 7. More preferably, the DNA includes the coding sequence of the nucleotides of SEQ ID NO: 6, or a degenerate variant of such a sequence.

"Substantially pure DNA" is DNA that is part of a milieu in which the DNA does not naturally occurs. The DNA can be obtained by virtue of separation (partial or total purification) of some or all of the molecules of that milieu, or by virtue of alteration of sequences that flank the claimed DNA. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, an autonomously replicating plasmid or virus, the

genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by polymerase chain reaction (PCR) or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence, e.g., a fusion protein. Also included is a recombinant DNA which includes a portion of the nucleotides listed in SEQ ID NO: 6 which encodes an alternative splice variant of TADG-14.

The present invention encompasses DNA that have at least about 70% sequence identity to the coding sequence of the nucleotides listed in SEQ ID NO: 6, preferably at least 75% (e.g. at least 80%); and most preferably at least 90%. The identity between two sequences is a direct function of the number of matching or identical positions. When a subunit position in both of the two sequences is occupied by the same monomeric subunit, e.g., if a given position is occupied by an adenine in each of two DNA molecules, then they are identical at that position. For example, if 7 positions in a sequence 10 nucleotides in length are identical to the corresponding positions in a second 10-nucleotide sequence, then the two sequences have 70% sequence identity. The length of

comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 100 nucleotides. Sequence identity is typically measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705).

The invention also includes DNA that hybridizes at high stringency to a probe containing at least 15 consecutive nucleotides of SEQ ID NO: 6. The probe to which the DNA of the invention hybridizes preferably consists of a sequence of at least 20 consecutive nucleotides, more preferably 40 nucleotides, even more preferably 50 nucleotides, and most preferably 100 nucleotides or more (up to 100%) of the coding sequence of the nucleotides listed in SEQ ID NO: 6 or the complement thereof. Such a probe is useful for detecting expression of TADG-14 in a cell by a method including the steps of (a) contacting mRNA obtained from the cell with the labeled hybridization probe; and (b) detecting hybridization of the probe with the mRNA.

By "high stringency" is meant DNA hybridization and wash conditions characterized by high temperature and low salt

concentration, e.g., wash conditions of 65°C at a salt concentration of approximately 0.1 x SSC, or the functional equivalent thereof. For example, high stringency conditions may include hybridization at about 42°C in the presence of about 50% formamide; a first wash at about 65°C with about 2 x SSC containing 1% SDS; followed by a second wash at about 65°C with about 0.1 x SSC.

The present invention further comprises a vector comprising a DNA sequence which encodes a human TADG-14 protein or a human TADG-14 variant protein. The vector comprises in operable linkage: a) an origin of replication; b) a promoter; and c) a DNA sequence coding for said protein. Preferably, the vector of the present invention contains a portion of the DNA sequence shown in SEQ ID No: 6 or encode a TADG-14 variant having the amino acid sequence of SEQ ID NO. 75.

A "vector" may be defined as a replicable nucleic acid construct, e.g., a plasmid or viral nucleic acid. Vectors may be used to amplify and/or express nucleic acid encoding TADG-14 protein. An "expression vector" is a replicable construct in which a nucleic acid sequence encoding a polypeptide is operably linked to suitable control sequences capable of effecting expression of the polypeptide in a cell. The need for such control sequences will vary depending

upon the cell selected and the transformation method chosen. Generally, control sequences include a transcriptional promoter and/or enhancer, suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation. Methods which are well known to those skilled in the art can be used to construct expression vectors containing appropriate transcriptional and translational control signals. See for example, the techniques described in Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual* (2nd Ed.), Cold Spring Harbor Press, N.Y. A gene and its transcription control sequences are defined as being "operably linked" if the transcription control sequences effectively control the transcription of the gene. Vectors of the invention include, but are not limited to, plasmid vectors and viral vectors. Preferred viral vectors of the invention are those derived from retroviruses, adenovirus, adeno-associated virus, SV40 virus, or herpes viruses.

A "heterologous' region of the DNA construct is an identifiable segment of DNA within a larger DNA molecule that is not found in association with the larger molecule in nature. Thus, when the heterologous region encodes a mammalian gene, the gene will usually be flanked by DNA that does not flank the mammalian

genomic DNA in the genome of the source organism. In another example, coding sequence is a construct where the coding sequence itself is not found in nature (e.g., a cDNA where the genomic coding sequence contains introns, or synthetic sequences having codons different than the native gene). Allelic variations or naturally-occurring mutational events do not give rise to a heterologous region of DNA as defined herein.

Further included in this invention are substantially pure TADG-14 protein or TADG-14 variant protein which are encoded at least in part by portions of SEQ ID NO. 7 and SEQ ID NO. 75 respectively. The protein products include alternative mRNA splicing or alternative protein processing events, or in which a section of TADG-14 sequence has been deleted. The fragment, or the intact TADG-14 polypeptide, may be covalently linked to another polypeptide, e.g. which acts as a label, a ligand or a means to increase antigenicity.

By a "substantially pure protein" is meant a protein which has been separated from at least some of those components which naturally accompany it. Typically, the protein is substantially pure when it is at least 60% by weight free from the proteins and other naturally-occurring organic molecules with which it is

naturally associated *in vivo*. Preferably, the purity of the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight. A substantially pure TADG-14 protein or TADG-14 variant may be obtained, for example, by extraction from a natural source; by expression of a recombinant nucleic acid encoding a TADG-14 or TADG-14 variant polypeptide; or by chemically synthesizing the protein. Purity can be measured by any appropriate method, e.g., column chromatography such as immunoaffinity chromatography using an antibody specific for TADG-14 or TADG-14 variant , polyacrylamide gel electrophoresis, or HPLC analysis. A protein which is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be, by definition, substantially free from its naturally associated components. Accordingly, substantially pure proteins include eukaryotic proteins synthesized in *E. coli*, other prokaryotes, or any other organism in which they do not naturally occur.

In addition to substantially full-length proteins, the invention also includes fragments (e.g., antigenic fragments) of the TADG-14 or TADG-14 variant protein. As used herein, "fragment," as applied to a polypeptide, will ordinarily be at least 10 residues,

more typically at least 20 residues, and preferably at least 30 (e.g., 50) residues in length, but less than the entire, intact sequence. Fragments of the TADG-14 or TADG-14 variant protein can be generated by methods known to those skilled in the art, e.g., by enzymatic digestion of naturally occurring or recombinant TADG-14 or TADG-14 variant protein, by recombinant DNA techniques using an expression vector that encodes a defined fragment of TADG-14 or TADG-14 variant, or by chemical synthesis. The ability of a candidate fragment to exhibit a characteristic of TADG-14 (e.g., binding to an antibody specific for TADG-14) can be assessed by methods described herein. Purified TADG-14 or antigenic fragments of TADG-14 can be used to generate new antibodies or to test existing antibodies (e.g., as positive controls in a diagnostic assay) by employing standard protocols known to those skilled in the art.

Included in this invention are polyclonal or monoclonal antibodies specific for TADG-14 or TADG-14 variant. Standard protocols for monoclonal and polyclonal antibody production known to those skilled in this art are employed. The monoclonal antibodies generated by this procedure can be screened for the ability to identify recombinant TADG-14 cDNA clones, and to distinguish them from known cDNA clones.

The invention encompasses not only an intact polyclonal or monoclonal antibody, but also an immunologically-active antibody fragment that recognizes TADG-14 or TADG-14 variant, e.g., a Fab or $(Fab)_2$ fragment; an engineered single chain Fv molecule; or a chimeric antibody in which the antigen binding sites are derived from murine antibody while the remaining portions of the antibody are of human origin.

In one embodiment, the antibody, or a fragment thereof, may be linked to a toxin or to a detectable label, e.g. a radioactive label, non-radioactive isotopic label, fluorescent label, chemiluminescent label, paramagnetic label, enzyme label, or colorimetric label. Examples of suitable toxins include diphtheria toxin, *Pseudomonas* exotoxin A, ricin, and cholera toxin. Examples of suitable enzyme labels include malate hydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, acetylcholinesterase, etc. Examples of suitable radioisotopic labels include ^{3}H, ^{125}I, ^{131}I, ^{32}P, ^{35}S, ^{14}C, etc.

Paramagnetic isotopes for purposes of *in vivo* diagnosis can also be used according to the methods of this invention. There are numerous examples of elements that are useful in magnetic resonance imaging. For discussions on *in vivo* nuclear magnetic resonance imaging, see, for example, Schaefer et al., (1989) *JACC* 14, 472-480; Shreve et al., (1986) *Magn. Reson. Med.* 3, 336-340; Wolf, G. L., (1984) *Physiol. Chem. Phys. Med. NMR* 16, 93-95; Wesbey et al., (1984) *Physiol. Chem. Phys. Med. NMR* 16, 145-155; Runge et al., (1984) *Invest. Radiol.* 19, 408-415. Examples of suitable fluorescent labels include a fluorescein label, an isothiocyalate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an ophthaldehyde label, a fluorescamine label, etc. Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, an aequorin label, etc.

Those of ordinary skill in the art will know of other suitable labels which may be employed in accordance with the present invention. The binding of these labels to antibodies or fragments thereof can be accomplished using standard techniques

commonly known to those of ordinary skill in the art. Typical techniques are described by Kennedy et al., (1976) *Clin. Chim. Acta* 70, 1-31; and Schurs et al., (1977) *Clin. Chim. Acta* 81, 1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method. All of these methods are incorporated by reference herein.

As described herein, the invention provides a number of diagnostic advantages and uses. For example, the TADG-14 or TADG-14 variant protein is useful in diagnosing cancer in different tissues since this protein is absent in highly proliferating cells. Antibodies (or antigen-binding fragments thereof) which bind to an epitope specific for TADG-14 or TADG-14 variant are useful in a method of detecting TADG-14 protein in a biological sample for diagnosis of cancerous or neoplastic transformation. This method includes the steps of obtaining a biological sample (e.g., cells, blood, plasma, tissue, etc.) from a patient suspected of having cancer, contacting the sample with a labelled antibody (e.g., radioactively tagged antibody) specific for TADG-14 or TADG-14 variant, and detecting the TADG-14 protein using standard immunoassay techniques such as an ELISA. Antibody binding to the biological

sample indicates that the sample contains a component which specifically binds to an epitope within TADG-14.

Likewise, a standard Northern blot assay can be used to ascertain the relative amounts of TADG-14 or TADG-14 variant mRNA in a cell or tissue obtained from a patient suspected of having cancer. Northern assay usually uses a hybridization probe, e.g. a full-length, single stranded radiolabelled TADG-14 cDNA probe having a sequence complementary to SEQ ID NO: 6, or a fragment of that DNA sequence at least 20 (preferably at least 30, more preferably at least 50, and most preferably at least 100) consecutive nucleotides in length. The DNA hybridization probe can be labelled by any of the many different methods known to those skilled in this art.

In another embodiment of the present invention, there is provided a method of inhibiting expression of TADG-14 in a cell, comprising the step of: (a) introducing a vector into a cell, whereupon expression of the vector produces TADG-14 antisense DNA which hybridizes to endogenous TADG-14 mRNA and inhibits expression of TADG-14 in the cell.

Further embodied by the present invention, there is provided a method of inhibiting a TADG-14 protein in a cell,

comprising the step of: (a) introducing an antibody specific for TADG-14 protein or a fragment thereof into a cell, whereupon binding of the antibody to the TADG-14 protein inhibits the TADG-14 protein in said cell.

The present invention is also directed toward a method of targeted therapy to an individual, comprising the step of: (a) administering a compound having a targeting moiety and a therapeutic moiety to an individual, wherein the targeting moiety is specific for TADG-14. Representative targeting moieties are an antibody specific for TADG-14 and a ligand or ligand binding domain that binds TADG-14. Likewise, a representative therapeutic moiety is a radioisotope, a toxin, a chemotherapeutic agent and immune stimulants. Typically, the above-described method is useful when the individual suffers from ovarian cancer, breast cancer or cancers of the prostate, lung, colon and cervix.

The present invention also provides methods of diagnosing cancer in an individual, comprising the steps of: (a) obtaining a biological sample from an individual; and (b) detecting TADG-14 or TADG-14 variant in the sample. Generally, the presence of TADG-14 or TADG-14 variant in the sample is indicative of the presence of carcinoma in the individual. Generally, the biological

sample is blood, ascites fluid, interstitial fluid, tumor tissue biopsy or tumor cells. Typical means of detecting TADG-14 or TADG-14 variant are by Northern blot, Western blot, PCR, dot blot, ELISA, radioimmunoassay, DNA chips or tumor cell labeling. This method may be useful in diagnosing cancers such as ovarian, breast, prostate and colon cancers.

In still yet another embodiment of the present invention, there is provided a method of vaccinating an individual against TADG-14 protein, comprising the step of (a) inoculating an individual with a TADG-14 protein or fragment thereof which lacks TADG-14 protease activity. Typically, inoculation with the TADG-14 protein or fragment thereof elicits an immune response in the individual, thereby vaccinating the individual against TADG-14. Generally, the individual has cancer, is suspected of having cancer or is at risk of getting cancer. Preferably, the TADG-14 fragment is a 9-residue fragment up to a 20-residue fragment, and more preferably, the 9-residue fragment is SEQ ID Nos. 17, 18, 41, 42, 47, 48, 53, 56, or 64.

In another embodiment of the present invention, there is provided a method of producing activated immune cells directed toward TADG-14, comprising the steps of exposing immune cells to

a TADG-14 protein or fragment thereof which lacks TADG-14 protease activity. Usually, exposure to the TADG-14 protein or fragment thereof activates the immune cells, thereby producing activated immune cells directed toward TADG-14. Generally, the immune cells are B cells, T cells or dendritic cells. Preferably, the dendritic cells are isolated from an individual prior to exposure to a TADG-14 protein or fragment thereof, and then reintroduced into the individual subsequent to the exposure. Typically, the individual has cancer, is suspected of having cancer or is at risk of getting cancer. Preferably, the TADG-14 fragment is a 9-residue fragment up to a 20-residue fragment, and more preferably, the 9-residue fragment is SEQ ID Nos. 17, 18, 41, 42, 47, 48, 53, 56, or 64.

In another embodiment of the present invention, there is provided an immunogenic composition, comprising an immunogenic fragment of a TADG-14 protein and an appropriate adjuvant. Preferably, the TADG-14 fragment is a 9-residue fragment up to a 20-residue fragment, and more preferably, the 9-residue fragment is SEQ ID Nos. 17, 18, 41, 42, 47, 48, 53, 56, or 64.

In another embodiment of the present invention, there is provided an oligonucleotide having a sequence complementary to SEQ ID No. 6, as well as a composition comprising the

oligonucleotide and a physiologically acceptable carrier. Additionally, there is provided a method of treating a neoplastic state in an individual in need of such treatment, comprising the step of (a) administering to the individual an effective dose of the above-described oligonucleotide.

The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion. One skilled in the art will appreciate readily that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those objects, ends and advantages inherent herein. Changes therein and other uses which are encompassed within the spirit of the invention as defined by the scope of the claims will occur to those skilled in the art.

EXAMPLE 1

Cloning and characterization of TADG-14

Tissue Collection And Storage

Upon patient hysterectomy, bilateral salpingo-oophorectomy, or surgical removal of neoplastic tissue, the specimen was retrieved and placed it on ice. The specimen was then taken to the resident pathologist for isolation and identification of specific tissue samples. Finally, the sample was frozen in liquid nitrogen, logged into the laboratory record and stored at -80°C. Additional specimens were frequently obtained from the Cooperative Human Tissue Network (CHTN). These samples were prepared by the Cooperative Human Tissue Network and shipped on dry ice. Upon arrival, these specimens were logged into the laboratory record and stored at -80°C.

mRNA Isolation And cDNA Synthesis

Messenger RNA (mRNA) isolation was performed according to the manufacturer's instructions using the Mini RiboSep™ Ultra mRNA isolation kit purchased from Becton Dickinson. This was an oligo(dT) chromatography based system of

mRNA isolation. The amount of mRNA recovered was quantitated by UV spectrophotometry.

First strand complementary DNA (cDNA) was synthesized using 5.0 ug of mRNA and either random hexamer or oligo(dT) primers according to the manufacturer's protocol utilizing a first strand synthesis kit obtained from Clontech. The purity of the cDNA was evaluated by PCR using primers specific for the p53 gene. These primers span an intron such that pure cDNA can be distinguished from cDNA that is contaminated with genomic DNA.

PCR Reactions

Reactions with degenerate primers and quantitative PCR reactions were carried out as previously described (10,11). The sequences of the TADG-14 specific primers that produce the 230 bp product were as follows: 5'-ACAGTACGCCTGGGAGACCA-3' (SEQ ID No. 12) and 5'-CTGAGACGGTGCAATTCTGG-3' (SEQ ID No. 13).

T-Vector Ligation And Transformations

The purified PCR products were ligated into the Promega T-vector plasmid and the ligation products were used to transform JM109 competent cells according to the manufacturer's

instructions. Positive colonies were cultured for amplification, the plasmid DNA isolated by means of the Wizard™ Minipreps DNA purification system, and the plasmids were digested with ApaI and SacI restriction enzymes to determine the size of the insert. Plasmids with inserts of the size(s) visualized by the previously described PCR product gel electrophoresis were sequenced.

DNA Sequencing

Utilizing a plasmid specific primer near the cloning site, sequencing reactions were carried out using PRISM™ Ready Reaction Dye Deoxy™ terminators (Applied Biosystems) according to the manufacturer's instructions. Residual dye terminators were removed from the completed sequencing reaction using a Centri-sep™ spin column (Princeton Separation). An Applied Biosystems Model 373A DNA Sequencing System was used for sequence analysis. Sequences were compared to GenEMBL databases using the FASTA program (Wisconsin Package Version 9.1, Genetics Computer Group (GCG), Madison, Wisconsin.) Multiple sequence alignments were generated with the Bestfit and Pileup programs available through Genetics Computer Group.

Northern Blot Analysis

mRNAs (approximately 5 μg) were size separated by electrophoresis through a 6.3% formaldehyde, 1.2% agarose gel in 0.02 M MOPS, 0.05 M sodium acetate (pH 7.0), and 0.001 M EDTA. The mRNAs were then blotted to Hybond-N (Amersham) by capillary action in 20x SSPE. The RNAs were fixed to the membrane by baking for 2 hours at 80°C. Additional multiple tissue northern (MTN) blots were purchased from CLONTECH Laboratories, Inc., including the Human multiple tissue northern blot (cat.#7760-1), the Human multiple tissue northern II blot (cat.#7759-1), the Human Fetal multiple tissue northern II blot (cat.#7756-1), and the Human Brain multiple tissue northern III blot (cat.#7750-1). The 230bp TADG-14 specific PCR product was radiolabelled utilizing the Prime-a-Gene Labelling System available from Promega. The blots were probed and stripped according to the ExpressHyb Hybridization Solution protocol available from CLONTECH.

Antibody Production And Western Blot Analysis

Polyclonal antibodies were generated by immunization of white New Zealand rabbits with one of three poly-lysine linked multiple antigen peptides derived from the deduced amino acid

sequence of TADG-14. These sequences are KYTVRLGDHSLQ (T14-1, SEQ ID No. 14), GHECQPHSQPWQ (T14-2, SEQ ID No. 15), and LDWIKKIIGSKG (T14-3, SEQ ID No. 16). For Western blot analysis, approximately 20 ug of MDA-MB-435S and HeLa cell lysates were separated on a 15% SDS-PAGE gel and electroblotted to PVDF at 100V for 40 minutes at 4°C. The blot was blocked overnight in Tris-buffered saline (TBS), pH 7.8 containing 0.2% non-fat milk. Primary antibody was added to the membrane at a dilution of 1:100 in 0.2% milk/TBS and incubated for 2 hours at room temperature. The blot was washed and incubated with a 1:3000 dilution of alkaline-phosphatase conjugated goat anti-rabbit IgG antibody (Bio-Rad) for one hour at room temperature. The blot was washed and incubated with a chemiluminescent substrate (Bio-Rad) before a 10-second exposure to X-ray film for visualization.

Immunohistochemistry

Immunohistochemical staining was performed using a Vectastain Elite ABC Kit (Vector). Formalin fixed and paraffin embedded specimens were routinely deparaffinized and processed using microwave heat treatment in 0.01 M sodium citrate buffer (pH 6.0). The specimens were incubated in methanol with 0.3% H_2O_2 for

30 minutes at room temperature and then incubated with normal goat serum for 30 minutes. The samples were incubated with anti-TADG-14 peptide derived polyclonal antibody for 1 hour at room temperature in a moisture chamber, followed by incubation with biotinylated anti-rabbit IgG for 30 minutes, and then incubated with ABC reagent (Vector) for 30 minutes. The final products were visualized using the AEC substrate system (DAKO) and sections were counter stained with hematoxylin before mounting. Negative controls were performed by using normal serum instead of the primary antibody.

Cloning Results

The gene encoding the novel extracellular serine protease of the present invention was identified from a group of proteases overexpressed in carcinoma by subcloning and sequencing the appropriate PCR products. An example of such a PCR reaction is given in Figure 1. Subcloning and sequencing of individual bands from such an amplification provided a basis for identifying the novel protease of the present invention.

After confirming the 406 bp PCR product was unique and was appropriately conserved to fit into the serine protease family,

this PCR product was used as a probe for Northern blot analysis to determine the transcript size and tissue specificity of its expression. It was found that the mRNA for this clone is approximately 1.4 kilobases (kb) (Fig. 2A), and that it is strongly expressed in ovarian carcinomas but not in normal ovary. More importantly, the transcript was found to be undetectable by Northern analysis in 28 normal human tissues studied (Fig. 2B, C, D and data not shown). In a more sensitive assay of 50 normal human tissues (Clontech), RNA dot blot analysis revealed that this clone was very weakly expressed in only three of these 50 tissues, kidney, lung and mammary gland (data not shown).

Using standard hybridization techniques, a cDNA library constructed from the mRNA isolated from the ascites cells of an ovarian cystadenocarcinoma patient was screened. Five clones were obtained, two of which overlapped and spanned 1343 nucleotides (Fig. 3A). The last two nucleotides prior to the poly (A) tail and the poly (A) tail itself were obtained from the EST database available at NCBI (accession #AA343629). Subsequent Northern blot analyses with probes derived from sequences near the 5' or 3' end of this cDNA were consistent with previous results suggesting that the obtained clones were produced by the same gene (data not shown).

This cDNA includes a Kozak's consensus sequence for the initiation of translation, and a polyadenylation signal.

The mRNA provides an open reading frame of 260 amino acids, which contains the necessary residues (His^{73}, Asp^{120}, Ser^{212}) in the appropriate context to classify this protein as a trypsin-like serine protease (1). Near its amino-terminus, the predicted protein contains a stretch of hydrophobic amino acids that probably serve as a secretion signal sequence. In addition, residues 110 to 112 encode a potential site for glycosylation that is common to serine proteases of the kallikrein subfamily such as PSA. This enzyme was named TADG-14, and the sequence was submitted to GenBank and assigned the accession # AF055982.

Comparison of the deduced TADG-14 amino acid sequence with sequences of known proteases revealed that it possesses significant similarity with human glandular kallikrein (hHk2), PSA, Protease M and mouse neuropsin (11-14). The sequence determined for the catalytic domain of TADG-14 is presented in Figure 4 and is consistent with other serine proteases and specifically contains conserved amino acids appropriate for the catalytic domain of the serine protease family. At the amino acid level TADG-14 is 48% identical to Protease M, 46% identical to

hHk2, and 43% identical to PSA (Fig. 3B). More interestingly, the mouse protease neuropsin and TADG-14 share 72% amino acid identity. In addition to the similarity of the protein sequences, neuropsin and TADG-14 mRNAs are of similar size (1.4 kb) and structure with approximately the same amounts of 5' and 3' untranslated regions suggesting the possibility of orthology. Neuropsin was originally identified as being expressed in mouse hippocampus and shown to be differentially expressed under stimulation (14). However, TADG-14 mRNA was undetectable in human whole brain by Northern blot. Further, Northern blot analysis for TADG-14 in eight separate parts of human brain including amygdala, caudate nucleus, corpus callosum, hippocampus, whole brain, substantia nigra, subthalamic nucleus and thalmus, also turned out to be negative. Recently, a human cDNA encoding neuropsin has been submitted to the GenBank database (accession # AB009849). Although this clone represents a different transcript from TADG-14, it encodes a protein that is identical to TADG-14 (15). Therefore, it seems logical that TADG-14 and neuropsin may arise as alternative splicing products from the same gene.

To characterize the extent and frequency of expression of the TADG-14 gene in ovarian tumors, semi-quantitative PCR was performed with cDNA derived from normal ovary, ovarian carcinoma or low malignant potential (LMP) tumors as template. This technique has been previously authenticated and verified by Northern blot, Western blot and immunohistochemistry (9, 16). PCR primers that amplify a TADG-14 specific 230 bp product were synthesized and used simultaneously in reactions with primers that produce a specific 454 bp PCR product for ß-tubulin. A radiolabelled nucleotide was included in this reaction, the PCR products were separated on a 2% agarose gel and the intensity of each band was quantitated by a Phosphoimager (Molecular Dynamics). Figure 5A shows an ethidium bromide stained agarose gel with the separated quantitative PCR products and is representative of the typical results observed.

The ratio of the TADG-14 PCR product to that of ß-tubulin (mean ± SD) was calculated for normal ovary samples which all showed relatively low expression levels (0.034 ± 0.024). TADG-14 overexpression was defined as exceeding the mean of the ratio of TADG-14 to ß-tubulin for normal samples by greater than 2 standard deviations (SD). TADG-14 was found to be overexpressed

in 4 of 10 LMP tumors (40%), and 20 of 30 ovarian carcinomas (67%) studied. For individual histologic subtypes of tumor, the expression ratio was 0.110 ± 0.092 for serous LMP tumors, 0.096 ± 0.142 for mucinous LMP tumors, 0.457 ± 0.345 for serous carcinomas, 0.171± 0.300 for mucinous carcinomas, 0.308 ± 0.144 for clear cell carcinomas, and 0.485 ± 0.325 for endometrioid carcinomas. Of the 30 ovarian carcinomas studied, 13 of 17 serous tumors, 1 of 7 mucinous tumors, 3 of 3 clear cell tumors and 3 of 3 endometrioid tumors overexpressed TADG-14 (Fig. 5B). These data are summarized in Table 1. Although not quantitated, transcripts for TADG-14 were also detectable in breast and colon carcinoma (Fig. 6).

TABLE 1

TADG-14 Overexpression by Tissue Subtype

Tissue Type		TADG14 Overexpression
Normal		0/10 (0%)
LMP		4/10 (40%)
	Serous	3/6 (50%)
	Mucinous	1/4 (25%)
Carcinoma		20/30 (67%)
	Serous	13/17 (76%)
	Mucinous	1/7 (14%)
	Endometri	3/3 (100%)
oid		
	Clear Cell	3/3 (100%)

Immunogenic poly-lysine linked multiple antigen peptides were synthesized based on the deduced amino acid sequence of TADG-14 and used to immunize rabbits for the production of polyclonal antibodies. The antiserum raised to the peptide sequence LDWIKKIIGSKG (SEQ ID No. 16), near the carboxy terminal (AA #249-260), was used in Western blot analysis to

determine if this antibody would recognize a protein of the predicted size of 28kDa. Proteins from the HeLa cell line and the carcinoma derived MD-MBA-435S cell line were used in this experiment and it was found that the antibody recognized a single 30 kDa protein in both cell lines (Fig. 7, lanes 3 and 4). This size is within a reasonable range of the predicted molecular weight. As a negative control, duplicate HeLa and MD-MB435S lysates were examined with rabbit pre-immune serum (Fig. 7, lanes 1 and 2). More importantly, this experiment was reproducible with antisera to a peptide from a different region of TADG-14, suggesting that these cultured cancer cells produce the TADG-14 protein.

Immunohistochemical staining supported the data obtained by quantitative PCR and Northern blot. Using a TADG-14 peptide directed antibody, no staining was observed with normal ovarian tissue samples (Figure 8A). However, intense staining was associated with tumor cells of all of the various histological subtypes of ovarian carcinoma examined. For serous carcinoma (Figure 8B and 8C) the antigen appears to be associated with tumor cells in the form of granules. These granular structures may be intermediates in the pathway that ultimately leads to secretion of TADG-14. In mucinous and clear cell carcinoma samples (Figures

8D and F respectively), TADG-14 is highly associated with the tumor cells. In endometrioid carcinoma (Figure 8E), the antigen is most prevalent in the glandular lumen formed by the tumor cells.

The lethality of neoplastic cells lies in their ability to proliferate abnormally and invade normal host tissues. Malignancies employ proteases to provide a variety of services that assist in the process of tumor progression including activation of growth and angiogenic factors and to provide the basis for invasion and metastasis. In the process of studying these enzymes, overexpression of known proteases such as hepsin and SCCE have been identified. In the present study, a cDNA encoding a novel serine protease, TADG14, was cloned. This protease was found to be very highly expressed in 67% (20/30) of ovarian carcinomas studied, whereas it was undetected in normal ovarian tissue. The TADG14 transcript was also not detectable in any of 50 normal human tissues studied. On prolonged Northern blot exposure, extremely low levels of TADG-14 were detected in normal kidney, breast and lung. This suggests the possibility that this gene is under the control of a promoter that is most active in ovarian tumors, and it may be possible to exploit this for therapeutic means. Unfortunately, TADG14 expression can be detected in other types of

cancer including prostate, breast and colon. This may limit the usefulness of TADG14 as a potential diagnostic maker for ovarian carcinoma, but it in no way detracts from the usefulness of this molecule as a target for cancer therapy or the usefulness of the TADG14 promoter in gene therapy applications.

At the nucleotide level, TADG14 mRNA resembles the recently cloned human neuropsin transcript with obvious differences residing in the 5' and 3' UTRS. TADG14 mRNA contains 491 bases of 5' UTR that were not found in human neuropsin. Also, the nucleotides preceding the poly (A) tail in the 3' UTR are not homologous. A 0.9kb transcript for human neuropsin was identified in cultured keratinocytes but not in normal hippocampus. Also, it was not identified as being associated with tumors. At the amino acid level, TADG14 is identical to human neuropsin.

Among other known proteases, TADG14 most closely resembles the mouse protease known as neuropsin, which was originally cloned from mouse hippocampus, and subsequently implicated in neuronal plasticity (17). If TADG14 functions in a manner similar to mouse neuropsin, it may be capable of restructuring the three-dimensional architecture of a tumor allowing for shedding of tumor cells or invasion of normal host

tissues by degrading fibronectin (18). In support of this, immunohistochemical staining of ovarian tumors revealed that TADG14 is highly associated with tumor cells and the cells near the invasive fronts of tumor. Therefore, TADG14 could be an important target for the inhibition of tumor progression.

Most importantly, the five-year survival rate for ovarian cancer patients remains below 50% because of an inability to diagnose this disease at an early stage. TADG14 contains a secretion signal sequence and immunohistochemical data suggest that TADG14 is secreted. In addition, by Northern blot and RNA dot blot analyses, TADG14 appears only in abundance in tumor tissues. As a result of this, it may be possible to design assays based on the detection of this protein for the early detection of ovarian cancer. Currently, the best available ovarian cancer tumor marker is CA125. However, due to high endogenous circulating levels of this antigen, the signal to noise ratio limits its usefulness as a diagnostic tool. Therefore, TADG14, due to its limited expression in other tissues and potential for being present in the circulation of tumor bearing patients, may prove to be a useful tool for early detection of ovarian cancer, especially the most prevalent serous cystadenocarcinoma subtype.

EXAMPLE 2

Peptide Ranking Analysis For Vaccine Candidates

For vaccine or immune stimulation, individual 9-mers to 11-mers of the TADG-14 protein were examined to rank the binding of individual peptides to the top 8 haplotypes in the general population (Parker et al., (1994)). Table 2 shows the peptide ranking based upon the predicted half-life of each peptide's binding to a particular HLA allele. A larger half-life indicates a stronger association with that peptide and the particular HLA molecule. The TADG-14 peptides that strongly bind to an HLA allele are putative immunogens, and are used to innoculate an individual against TADG-14.

TABLE 2

TADG-14 Peptide Ranking

HLA Type & Ranking	Start	Peptide	Predicted Dissociation$_{1/2}$	SEQ ID No.
HLA A0201				
1	55	QLLCGGVLV	257.342	17
2	15	LLLLGGAWA	171.868	18
3	60	GVLVGGNWV	123.846	19
4	61	VLVGGNWVL	111.672	20
5	49	ALFQGQQLL	79.041	21
6	10	KTWMFLLLL	75.331	22
7	131	SLGSKVKPI	23.995	23
8	122	MLLQLRDQA	15.312	24
9	124	LQLRDQASL	13.624	25
10	170	TLNCAEVKI	10.433	26
HLA A0205				
1	124	LQLRDQASL	28.560	25
2	10	KTWMFLLLL	25.200	22
3	49	ALFQGQQLL	21.000	21
4	208	CQGDSGGPL	16.800	27
5	54	QQLLCGGVL	16.800	28
6	61	VLVGGNWVL	14.280	20
7	60	GVLVGGNWV	12.000	19
8	62	LVGGNWVLT	6.800	29
9	55	QLLCGGVLV	6.000	17
10	191	QITDGMVCA	3.000	30
HLA A1				
1	173	CAEVKIFPQ	4.500	31
2	83	LGDHSLQNK	2.500	32
3	183	KCEDAYPGQ	1.800	33
4	192	ITDGMVCAG	1.250	34
5	71	AAHCKKPKY	1.000	35
6	113	DVEDHNHDL	0.900	36
7	229	GSDPCGRSD	0.750	37
8	111	SSDVEDHNH	0.750	38
9	28	AQEDKVLGG	0.675	39

	10	217	VCDGALQGI	0.500	40
	HLA A24				
	1	241	VYTNICRYL	280.000	41
	2	247	RYLDWIKKI	198.000	42
5	3	10	KTWMFLLLL	8.000	22
	4	7	RAAKTWMFL	8.000	43
	5	42	HSQPWQAAL	7.200	44
	6	48	AALFQGQQL	7.200	45
	7	113	DVEDHNHDL	7.200	36
10	8	54	QQLLCGGVL	6.000	28
	9	214	GPLVCDGAL	6.000	46
	10	61	VLVGGNWVL	6.000	20
	HLA B7				
	1	80	TVRLGDHSL	200.000	47
15	2	5	RPRAAKTWM	200.000	48
	3	214	GPLVCDGAL	80.000	46
	4	48	AALFQGQQL	36.000	45
	5	8	AAKTWMFLL	36.000	49
	6	3	RPRPRAAKT	20.000	50
20	7	162	SPRENFPDT	20.000	51
	8	188	YPGQITDGM	20.000	52
	9	7	RAAKTWMFL	12.000	43
	10	49	ALFQGQQLL	12.000	21
	HLA B8				
25	1	133	GSKVKPISL	80.000	53
	2	8	AAKTWMFLL	16.000	49
	3	3	RPRPRAAKT	8.000	50
	4	80	TVRLGDHSL	4.000	47
	5	73	HCKKPKYTV	2.400	54
30	6	131	SLGSKVKPI	2.000	23
	7	5	RPRAAKTWM	2.000	48
	8	162	SPRENFPDT	1.200	51
	9	214	GPLVCDGAL	0.800	46
	10	179	FPQKKCEDA	0.800	55
35	HLA B2702				
	1	234	GRSDKPGVY	200.000	56
	2	246	CRYLDWIKK	20.000	57

	3	101	VQSIPHPCY	20.000	58
	4	43	SQPWQAALF	20.000	59
	5	6	PRAAKTWMF	20.000	60
	6	26	SRAQEDKVL	18.000	61
	7	126	LRDQASLGS	10.000	62
	8	149	GQKCTVSGW	10.000	63
	9	124	LQLRDQASL	6.000	25
	10	54	QQLLCGGVL	6.000	28
HLA B4403					
	1	96	QEIPVVQSI	180.000	64
	2	71	AAHCKKPKY	13.500	35
	3	171	LNCAEVKIF	4.500	65
	4	184	CEDAYPGQI	4.000	66
	5	114	VEDHNHDLM	4.000	67
	6	101	VQSIPHPCY	2.250	68
	7	236	SDKPGVYTN	1.800	69
	8	164	RENFPDTLN	1.800	70
	9	174	AEVKIFPQK	1.600	71
	10	43	SQPWQAALF	1.500	59

EXAMPLE 3

TADG-14 Variant

Because members of the serine protease family are highly expressed and secreted by tumors, they offer potential targets for both diagnosis and therapy. While many of these enzymes are predominantly tumor produced, there is often some level of expression in a limited number of normal tissues. To further enhance the potential for more specific tumor diagnosis and

targeting, it would be helpful to provide unique sequences which might be included in the enzyme families. The present example discloses a transcription variant of TADG-14. The TADG-14 variant includes unique intron sequence which could provide potential specificity to the recognition of TADG-14 in tumor.

Data presented above indicated TADG-14 overexpression in ovarian tumors. Kishi et al. confirmed the overexpression of KLK8 (Neuropsin/Ovasin), which was described as TADG-14 here, as highly overexpressed in the ascites fluid of ovarian cancer patients and presented at elevated levels in serum of 62% of ovarian cancer patients.

When the complete transcript of the TADG-14 gene was examined for potential variants, one variant was detected which included intron sequence between exon 2 and exon 3. Using primers from exon 1 and exon 3 of TADG-14, a PCR band larger than the expected exon 2- exon 3 band was detected in ovarian tumor cells (Figure 9). The sequence of this TADG-14 variant was confirmed. It included all intron 2 sequence and it could be translated into an extended amino acid sequence which presumably would still have protease activity (Figures 10-11). The addition of the intron sequence and the subsequent translation into additional

amino acid sequence provides an opportunity to add unique specificity for diagnostic detection and/or targeting of tumor therapy. This variant was expressed in 5 out of 6 ovarian carcinomas examined. Normal ovary cells did not express this TADG-14 variant. On examination of the EST database for taq sequence for intron 2 of TADG-14, only one expressed sequence was detected in an adenocarcinoma cell line of the ovary. These data thus suggest a potential role for this TADG-14 variant in both detecting and targeting of ovarian carcinomas.

Sense and antisense primers were made to exons 2 and 3 of TADG-14 (TADG-14 Sense, 5'-CGA CCT CGT GCG GCC AAG ACG-3', SEQ ID NO. 73; TADG-14 Antisense, 5'-CAG CTG TAA GGA CCC AGT TGC-3', SEQ ID NO. 74). All PCR was run in 20 ul reactions consisting of ovarian tumor cDNA derived from 50 ng of mRNA, 5 pmol each of sense and antisense primers, 0.2 mmol of dNTPs, 2.5mmol of $MgCl_2$ and 1U of Taq polymerase in 1x buffer. This mixture was subjected to 1.5 minutes of denaturation at 94°C followed by 35 cycles of PCR consisting of the following: denaturation for 30 seconds at 94°C, 30 seconds of annealing at the appropriate temperature for each primer set, and 1 minute of extension at 72°C with an additional 7 minutes of extension on the

last cycle.

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Any patents or publications mentioned in this specification are indicative of the levels of those skilled in the art to which the invention pertains. These patents and publications are herein incorporated by reference to the same extent as if each individual publication was specifically and individually indicated to be incorporated by reference.